Chong, K.
C9/888164

FILE 'REGISTRY' ENTERED AT 10:16:03 ON 05 APR 2005
L1 64 S AAAGCCACCCAAGGCA/SQSN

FILE 'CAPLUS' ENTERED AT 10:22:58 ON 05 APR 2005
L2 32 S L1
L3 0 S L2 AND LIGAND

L2 ANSWER 1 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 18 Feb 2005
ACCESSION NUMBER: 2005:141225 CAPLUS
DOCUMENT NUMBER: 142:234475
TITLE: Double-stranded RNAs for inhibiting expression of hepatitis B virus and hepatitis C virus sequences, and therapeutic use thereof
INVENTOR(S): Pachuk, Catherine J.; Satishchandran, C.; Zurawski, Vincent R., Jr.; Mintz, Liat
PATENT ASSIGNEE(S): Nucleonics, Inc., USA
SOURCE: PCT Int. Appl., 123 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005014806	A2	20050217	WO 2004-US19229	20040610

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2003-478076P P 20030612

AB The invention provides conserved consensus sequences from known hepatitis B virus (HBV) strains and known hepatitis C virus (HCV) strains, which are useful in inhibiting the expression of the viruses in mammalian cells. These sequences are useful to silence the genes of HBV and HCV, thereby providing therapeutic utility against HBV and HCV viral infection in humans. Human liver-derived cell line Huh7 was co-transfected with an infectious HBV plasmid and various vectors that encode an HBV-targeting short hairpin RNA. The cells had a 30-50% reduction in hepatitis B surface antigen secretion. Two of the shRNA vectors were tested in a mouse model and both were found to silence the HBV replicon as shown by downregulation of surface antigen-specific HBV RNA and serum levels of hepatitis B surface antigens. The examples describe similar expts. for siRNAs that target the 3'-untranslated region of hepatitis C virus.

IT **148188-81-2**, GenBank V01460
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(double-stranded RNAs for inhibiting expression of hepatitis B

virus and hepatitis C virus sequences, and therapeutic use thereof)

L2 ANSWER 2 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 25 Jan 2005
ACCESSION NUMBER: 2005:64153 CAPLUS
DOCUMENT NUMBER: 142:170782
TITLE: The repetitive landscape of the chicken genome
AUTHOR(S): Wicker, Thomas; Robertson, Jon S.; Schulze, Stefan R.; Feltus, F. Alex; Magrini, Vincent; Morrison, Jason A.; Mardis, Elaine R.; Wilson, Richard K.; Peterson, Daniel G.; Paterson, Andrew H.; Ivarie, Robert
CORPORATE SOURCE: Plant Genome Mapping Laboratory, University of Georgia, Athens, GA, 30602, USA
SOURCE: Genome Research (2005), 15(1), 126-136
CODEN: GEREFS; ISSN: 1088-9051
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Cot-based cloning and sequencing (CBCS) is a powerful tool for isolating and characterizing the various repetitive components of any genome, combining the established principles of DNA reassocn. kinetics with high-throughput sequencing. CBCS was used to generate sequence libraries representing the high, middle, and low-copy fractions of the chicken genome. Sequencing high-copy DNA of chicken to about 2.7 + coverage of its estimated sequence complexity led to the initial identification of several new repeat families, which were then used for a survey of the newly released first draft of the complete chicken genome. The anal. provided insight into the diversity and biol. of known repeat structures such as CR1 and CNM, for which only limited sequence data had previously been available. Cot sequence data also resulted in the identification of four novel repeats (Birddawg, Hitchcock, Kronos, and Soprano), two new subfamilies of CR1 repeats, and many elements absent from the chicken genome assembly. Multiple autonomous elements were found for a novel Mariner-like transposon, Galluhop, in addition to nonautonomous deletion derivs. Phylogenetic anal. of the high-copy repeats CR1, Galluhop, and Birddawg provided insight into two distinct genome dispersion strategies. This study also exemplifies the power of the CBCS method to create representative databases for the repetitive fractions of genomes for which only limited sequence data is available. A total of 15,103 genome survey sequences are deposited in GenBank/EMBL/DDBJ under accession nos. CL266240-CL281342. [This abstract record is one of four records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].
IT **833920-72-2**, GenBank CL272028
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; repetitive landscape of the chicken genome)

L2 ANSWER 3 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 21 Dec 2004
ACCESSION NUMBER: 2004:1099774 CAPLUS
DOCUMENT NUMBER: 142:18286
TITLE: Development of an expressed sequence tag (EST) resource for wheat (Triticum aestivum L.): EST generation, unigene analysis, probe selection and bioinformatics for a 16,000-locus bin-delineated map of wheat

AUTHOR(S): Lazo, G. R.; Chao, S.; Hummel, D. D.; Edwards, H.; Crossman, C. C.; Lui, N.; Matthews, D. E.; Carollo, V. L.; Hane, D. L.; You, F. M.; Butler, G. E.; Miller, R. E.; Close, T. J.; Peng, J. H.; Lapitan, N. L. V.; Gustafson, J. P.; Qi, L. L.; Echalier, B.; Gill, B. S.; Dilbirligi, M.; Randhawa, H. S.; Gill, K. S.; Greene, R. A.; Sorrells, M. E.; Akhunov, E. D.; Dvorak, J.; Linkiewicz, A. M.; Dubcovsky, J.; Hossain, K. G.; Kalavacharla, V.; Kianian, S. F.; Mahmoud, A. A.; Miftahudin; Ma, X.-F.; Conley, E. J.; Anderson, J. A.; Pathan, M. S.; Nguyen, H. T.; McGuire, P. E.; Qualset, C. O.; Anderson, O. D.

CORPORATE SOURCE: Western Regional Research Center, U.S. Department of Agriculture-Agricultural Research Service (USDA-ARS), Albany, CA, 94710-1105, USA

SOURCE: Genetics (2004), 168(2), 585-593
CODEN: GENTAE; ISSN: 0016-6731

PUBLISHER: Genetics Society of America

DOCUMENT TYPE: Journal

LANGUAGE: English

AB This report describes the rationale, approaches, organization, and resource development leading to a large-scale deletion bin map of the hexaploid (2n = 6x = 42) wheat genome (Triticum aestivum). Accompanying reports detail results from chromosome bin-mapping of expressed sequence tags (ESTs) representing genes onto the 7 homoeologous chromosome groups and a global anal. of the entire mapped wheat EST data set. Among the resources developed were the first extensive public wheat EST collection (113,220 ESTs). Described are protocols for sequencing, sequence processing, EST nomenclature, and the assembly of ESTs into contigs. These contigs plus singletons (unassembled ESTs) were used for selection of distinct sequence motif unigenes. Selected ESTs were rearrayed, validated by 5' and 3' sequencing, and amplified for probing a series of wheat aneuploid and deletion stocks. Images and data for all Southern hybridizations were deposited in databases and were used by the coordinators for each of the 7 homoeologous chromosome groups to validate the mapping results. Results from this project have established the foundation for future developments in wheat genomics. [This abstract record is one of thirty records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **423908-16-1**, GenBank BQ283554
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; EST generation, unigene anal., probe selection and bioinformatics for a 16,000-locus bin-delineated map of wheat)

L2 ANSWER 4 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 12 Apr 2004
ACCESSION NUMBER: 2004:293983 CAPLUS
DOCUMENT NUMBER: 141:65785
TITLE: Quantitative assay system established for different hepatitis B virus RNAs in sera sample
AUTHOR(S): Zhang, Wei; Su, Qin; Liu, Jie; Hacker, Hans J.; Niu, Yun; Liang, Xiufen; Schroeder, Claus H.
CORPORATE SOURCE: Tangdu Hospital, Fourth Military Medical University, Xian, Shanxi Province, 710038, Peop.

Rep. China
SOURCE: Disi Junyi Daxue Xuebao (2003), 24(8), 673-677
CODEN: DJDXEG; ISSN: 1000-2790
PUBLISHER: Disi Junyi Daxue Xuebao Bianjibu
DOCUMENT TYPE: Journal
LANGUAGE: Chinese

AB A quant. system to characterize different RNA mols. (transcripts) of hepatitis B virus (HBV) in circulation was established. Viral nucleic acids were extracted from serum samples and HBV DNA and RNA were characterized quant. by competitive PCR and RT-PCR procedures. A seroassay was established to characterize 3'-end structure of the full-length and truncated viral transcripts. Copy nos. of viral RNA/DNA segments corresponding to X, Core and X-Precore regions were determined, representing early, middle and late stages of HBV gene replication, resp. In addition, the data demonstrate dynamic changes in the circulating viral transcripts as well as DNA in their copy nos. and structures during lamivudine therapy. After a 8-wk treatment, the copy nos. for C or PreC/X DNA segments decreased to 105 · mL-1 from 109.mL-1, significantly below that for X segment (from 109 · mL-1 to 107 · mL-1). There was no significant decrease in RNA copy nos. Polyadenylated HBV RNA was also determined using anchored oligo (dT) primers targeting fRNA and trRNA. The copy nos. of fRNA and trRNA were 105 copies per mL of serum during most of the treatment period, significantly below that of X segment (107 · mL-1). The excess of X segment RNA over fRNA levels suggested a packaging-related removal of poly (A) 3'-ends. An assay for the detection of copy nos. and different 3' end structures of the circulating HBV transcripts is established, which provides a more precise approach to the detection of dynamic change of circulating HBV transcripts.

IT **709063-06-9**
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequences; assay system for hepatitis B virus RNAs in sera sample)

L2 ANSWER 5 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 08 Feb 2004
ACCESSION NUMBER: 2004:101279 CAPLUS
DOCUMENT NUMBER: 140:158524
TITLE: Partially double stranded RNAs with hairpin structures for use in RNA interference without induction of RNA-associated toxicity and their therapeutic uses
INVENTOR(S): Pachuk, Catherine J.; Satishchandran, C.; Chopra, Maninder; Shuey, David
PATENT ASSIGNEE(S): Nucleonics, Inc., USA
SOURCE: PCT Int. Appl., 174 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004011624	A2	20040205	WO 2003-US24028	20030731
WO 2004011624	C2	20040408		

WO 2004011624 A3 20041209
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.: US 2002-399998P P 20020731

AB Partially double-stranded interfering RNAs that include a hairpin structure are described for use in RNA interference. These interfering RNAs specifically inhibit the expression of target genes in a cell or animal without inducing the toxic effects, such as the RNA stress response, seen with prior art interfering RNAs. These methods can be used to prevent or treat a disease or infection by silencing a gene associated with the disease or infection. The invention also provides methods for identifying nucleic acid sequences that modulate a detectable phenotype, such as the function of a cell, the expression of a gene, or the biol. activity of a target polypeptide.

IT **148188-81-2**, GenBank V01460
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(partially double stranded RNAs with hairpin structures for use in RNA interference without induction of RNA-associated toxicity and their therapeutic uses)

L2 ANSWER 6 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 16 Jan 2004
ACCESSION NUMBER: 2004:39697 CAPLUS
DOCUMENT NUMBER: 140:123703
TITLE: Human prostate cancer marker genes associated with various metastatic stages identified by gene profiling, and related compositions, kits, and methods for diagnosis, prognosis and therapy
INVENTOR(S): Schlegel, Robert; Endege, Wilson O.
PATENT ASSIGNEE(S): Millennium Pharmaceuticals, Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 131 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004009481	A1	20040115	US 2002-166883	20020611
US 2004009481	A1	20040115	US 2002-166883	20020611
US 2004009481	A1	20040115	US 2002-166883	20020611
US 2004009481	A1	20040115	US 2002-166883	20020611
US 2004009481	A1	20040115	US 2002-166883	20020611

PRIORITY APPLN. INFO.: US 2001-297285P P 20010611
US 2002-166883 A 20020611

AB The invention relates to compns., kits, and methods for diagnosing, staging, prognosing, monitoring and treating human prostate cancers. A variety of marker genes are provided, wherein changes in the levels of expression of one or more of the marker genes is correlated with the presence of prostate cancer. In particular, three sets of the marker genes set, corresponding to 11617 GenBank Accession Nos. (only 2168 new submissions) and 15 SEQ IDs, are identified by transcription profiling using RNA derived from clin. samples, that were expressed at least 2-fold or greater than the normal controls. Using TNM staging approach, these markers are divided to three groups, ones can be used to determine whether prostate cancer has metastasized, or is likely to metastasize, to the liver (M stage); ones can be used to determine whether prostate cancer has metastasized, or is likely to metastasize, to the bone (M stage); and ones can be used to determine whether prostate cancer has metastasized, or is likely to metastasize, to the lymph nodes (N stage and/or M stage). The invention also relates to a kit for assessing the specific type of metastatic prostate cancer, e.g., cancer that has metastasized to the liver, bone or lymph nodes. [This abstract record is one of three records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **389735-54-0**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; human prostate cancer marker genes associated with various metastatic stages identified by gene profiling, and related compns., kits, and methods for diagnosis, prognosis and therapy)

L2 ANSWER 7 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 09 Jan 2004
ACCESSION NUMBER: 2004:14433 CAPLUS
DOCUMENT NUMBER: 140:106239
TITLE: Analysis and functional annotation of an expressed sequence tag collection for tropical crop sugarcane
AUTHOR(S): Vettore, Andre L.; da Silva, Felipe R.; Kemper, Edson L.; Souza, Glaucia M.; da Silva, Aline M.; Ferro, Maria Ines T.; Henrique-Silva, Flavio; Giglioti, Eder A.; Lemos, Manoel V. F.; Coutinho, Luiz L.; Nobrega, Marina P.; Carrer, Helaine; Franca, Suzelei C.; Bacci, Mauricio, Jr.; Goldman, Maria Helena S.; Gomes, Suely L.; Nunes, Luiz R.; Camargo, Luis E. A.; Siqueira, Walter J.; Van Sluys, Marie-Anne; Thiemann, Otavio H.; Kuramae, Eiko E.; Santelli, Roberto V.; Marino, Celso L.; Targon, Maria L. P. N.; Ferro, Jesus A.; Silveira, Henrique C. S.; Marini, Danyelle C.; Lemos, Eliana G. M.; Monteiro-Vitorello, Claudia B.; Tambor, Jose H. M.; Carraro, Dirce M.; Roberto, Patricia G.; Martins, Vanderlei G.; Goldman, Gustavo H.; de Oliveira, Regina C.; Truffi, Daniela; Colombo, Carlos A.; Rossi, Magdalena; de Araujo, Paula G.; Sculaccio, Susana A.; Angella, Aline; Lima, Marleide M. A.; de Rosa, Vicente E., Jr.; Siviero, Fabio; Coscrato, Virginia E.; Machado, Marcos A.; Grivet, Laurent; Di Mauro, Sonia M. Z.; Nobrega, Francisco G.; Menck, Carlos F. M.; Braga, Marilia

D. V.; Telles, Guilherme P.; Cara, Frank A. A.; Pedrosa, Guilherme; Meidanis, Joao; Arruda, Paulo
CORPORATE SOURCE: Centro de Biologia Molecular e Engenharia Genetica, Instituto da Computacao, Universidade Estadual de Campinas, Campinas, 13083-970, Brazil
SOURCE: Genome Research (2003), 13(12), 2725-2735
CODEN: GEREFS; ISSN: 1088-9051
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB To contribute to the understanding of the genome complexity of sugarcane, a large-scale expressed sequence tag (EST) program was undertaken. More than 260,000 cDNA clones were partially sequenced from 26 standard cDNA libraries generated from different sugarcane tissues. After the processing of the sequences, 237,954 high-quality ESTs were identified. These ESTs were assembled into 43,141 putative transcripts. Of the assembled sequences, 35.6% presented no matches with existing sequences in public databases. A global anal. of the whole SUCEST data set indicated that 14,409 assembled sequences (33% of the total) contained at least one cDNA clone with a full-length insert. Annotation of the 43,141 assembled sequences associated almost 50% of the putative identified sugarcane genes with protein metabolism, cellular communication/signal transduction, bioenergetics, and stress responses. Inspection of the translated assembled sequences for conserved protein domains revealed 40,821 amino acid sequences with 1415 Pfam domains. Reassembling the consensus sequences of the 43,141 transcripts revealed a 22% redundancy in the first assembling. This indicated that possibly 33,620 unique genes had been identified and indicated that >90% of the sugarcane expressed genes were tagged. [This abstract record is one of sixty records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **595461-40-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; anal. and functional annotation of an expressed sequence tag collection for tropical crop sugarcane)

L2 ANSWER 8 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 06 Jan 2004
ACCESSION NUMBER: 2004:6619 CAPLUS
DOCUMENT NUMBER: 140:88522
TITLE: Analysis and functional annotation of an expressed sequence tag collection for tropical crop sugarcane
AUTHOR(S): Vettore, Andre L.; da Silva, Felipe R.; Kemper, Edson L.; Souza, Glaucia M.; da Silva, Aline M.; Ferro, Maria Ines T.; Henrique-Silva, Flavio; Giglioti, Eder A.; Lemos, Manoel V. F.; Coutinho, Luiz L.; Nobrega, Marina P.; Carrer, Helaine; Franca, Suzelei C.; Bacci, Mauricio, Jr.; Goldman, Maria Helena S.; Gomes, Suely L.; Nunes, Luiz R.; Camargo, Luis E. A.; Siqueira, Walter J.; Van Sluys, Marie-Anne; Thiemann, Otavio H.; Kuramae, Eiko E.; Santelli, Roberto V.; Marino, Celso L.; Targon, Maria L. P. N.; Ferro, Jesus A.; Silveira, Henrique C. S.; Marini, Danyelle C.; Lemos, Eliana G. M.; Monteiro-Vitorello, Claudia B.; Tambor, Jose H. M.; Carraro, Dirce M.; Roberto, Patricia

G.; Martins, Vanderlei G.; Goldman, Gustavo H.; de Oliveira, Regina C.; Truffi, Daniela; Colombo, Carlos A.; Rossi, Magdalena; de Araujo, Paula G.; Sculaccio, Susana A.; Angella, Aline; Lima, Marleide M. A.; de Rosa, Vicente E., Jr.; Siviero, Fabio; Coscrato, Virginia E.; Machado, Marcos A.; Grivet, Laurent; Di Mauro, Sonia M. Z.; Nobrega, Francisco G.; Menck, Carlos F. M.; Braga, Marilia D. V.; Telles, Guilherme P.; Cara, Frank A. A.; Pedrosa, Guilherme; Meidanis, Joao; Arruda, Paulo

CORPORATE SOURCE: Centro de Biologia Molecular e Engenharia Genetica, Instituto da Computacao, Universidade Estadual de Campinas, Campinas, 13083-970, Brazil

SOURCE: Genome Research (2003), 13(12), 2725-2735
CODEN: GEREFS; ISSN: 1088-9051
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB To contribute to the understanding of the genome complexity of sugarcane, a large-scale expressed sequence tag (EST) program was undertaken. More than 260,000 cDNA clones were partially sequenced from 26 standard cDNA libraries generated from different sugarcane tissues. After the processing of the sequences, 237,954 high-quality ESTs were identified. These ESTs were assembled into 43,141 putative transcripts. Of the assembled sequences, 35.6% presented no matches with existing sequences in public databases. A global anal. of the whole SUCEST data set indicated that 14,409 assembled sequences (33% of the total) contained at least one cDNA clone with a full-length insert. Annotation of the 43,141 assembled sequences associated almost 50% of the putative identified sugarcane genes with protein metabolism, cellular communication/signal transduction, bioenergetics, and stress responses. Inspection of the translated assembled sequences for conserved protein domains revealed 40,821 amino acid sequences with 1415 Pfam domains. Reassembling the consensus sequences of the 43,141 transcripts revealed a 22% redundancy in the first assembling. This indicated that possibly 33,620 unique genes had been identified and indicated that >90% of the sugarcane expressed genes were tagged. [This abstract record is one of sixty records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **593230-84-3**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; anal. and functional annotation of an expressed sequence tag collection for tropical crop sugarcane)

L2 ANSWER 9 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 06 Jan 2004
ACCESSION NUMBER: 2004:6613 CAPLUS
DOCUMENT NUMBER: 140:88521
TITLE: Analysis and functional annotation of an expressed sequence tag collection for tropical crop sugarcane
AUTHOR(S): Vettore, Andre L.; da Silva, Felipe R.; Kemper, Edson L.; Souza, Glaucia M.; da Silva, Aline M.; Ferro, Maria Ines T.; Henrique-Silva, Flavio; Giglioti, Eder A.; Lemos, Manoel V. F.; Coutinho, Luiz L.; Nobrega, Marina P.; Carrer, Helaine; Franca, Suzelei C.; Bacci, Mauricio, Jr.; Goldman,

Maria Helena S.; Gomes, Suely L.; Nunes, Luiz R.; Camargo, Luis E. A.; Siqueira, Walter J.; Van Sluys, Marie-Anne; Thiemann, Otavio H.; Kuramae, Eiko E.; Santelli, Roberto V.; Marino, Celso L.; Targon, Maria L. P. N.; Ferro, Jesus A.; Silveira, Henrique C. S.; Marini, Danyelle C.; Lemos, Eliana G. M.; Monteiro-Vitorello, Claudia B.; Tambor, Jose H. M.; Carraro, Dirce M.; Roberto, Patricia G.; Martins, Vanderlei G.; Goldman, Gustavo H.; de Oliveira, Regina C.; Truffi, Daniela; Colombo, Carlos A.; Rossi, Magdalena; de Araujo, Paula G.; Sculaccio, Susana A.; Angella, Aline; Lima, Marleide M. A.; de Rosa, Vicente E., Jr.; Siviero, Fabio; Coscrato, Virginia E.; Machado, Marcos A.; Grivet, Laurent; Di Mauro, Sonia M. Z.; Nobrega, Francisco G.; Menck, Carlos F. M.; Braga, Marilia D. V.; Telles, Guilherme P.; Cara, Frank A. A.; Pedrosa, Guilherme; Meidanis, Joao; Arruda, Paulo

CORPORATE SOURCE: Centro de Biologia Molecular e Engenharia Genetica, Instituto da Computacao, Universidade Estadual de Campinas, Campinas, 13083-970, Brazil

SOURCE: Genome Research (2003), 13(12), 2725-2735
CODEN: GEREFS; ISSN: 1088-9051
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB To contribute to the understanding of the genome complexity of sugarcane, a large-scale expressed sequence tag (EST) program was undertaken. More than 260,000 cDNA clones were partially sequenced from 26 standard cDNA libraries generated from different sugarcane tissues. After the processing of the sequences, 237,954 high-quality ESTs were identified. These ESTs were assembled into 43,141 putative transcripts. Of the assembled sequences, 35.6% presented no matches with existing sequences in public databases. A global anal. of the whole SUCEST data set indicated that 14,409 assembled sequences (33% of the total) contained at least one cDNA clone with a full-length insert. Annotation of the 43,141 assembled sequences associated almost 50% of the putative identified sugarcane genes with protein metabolism, cellular communication/signal transduction, bioenergetics, and stress responses. Inspection of the translated assembled sequences for conserved protein domains revealed 40,821 amino acid sequences with 1415 Pfam domains. Reassembling the consensus sequences of the 43,141 transcripts revealed a 22% redundancy in the first assembling. This indicated that possibly 33,620 unique genes had been identified and indicated that >90% of the sugarcane expressed genes were tagged. [This abstract record is one of sixty records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **593230-84-3**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; anal. and functional annotation of an expressed sequence tag collection for tropical crop sugarcane)

L2 ANSWER 10 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 07 Nov 2003
ACCESSION NUMBER: 2003:874771 CAPLUS
DOCUMENT NUMBER: 139:358726
TITLE: RNA interference-mediated inhibition of hepatitis

	B virus (HBV) gene expression using short interfering nucleic acid (siNA)
INVENTOR(S):	Morrissey, David; Mcswiggen, James A.; Beigelman, Leonid
PATENT ASSIGNEE(S):	USA
SOURCE:	U.S. Pat. Appl. Publ., 72 pp., Cont.-in-part of Appl. No. PCT/US02/09187. CODEN: USXXCO
DOCUMENT TYPE:	Patent
LANGUAGE:	English
FAMILY ACC. NUM. COUNT:	144
PATENT INFORMATION:	

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003206887	A1	20031106	US 2002-244647	20020916
US 6017756	A	20000125	US 1994-193627	19940207
AU 9851819	A1	19980611	AU 1998-51819	19980112
AU 729657	B2	20010208		
AU 9939188	A1	19990916	AU 1999-39188	19990713
AU 769175	B2	20040115	AU 2000-56616	20000911
US 2003068301	A1	20030410	US 2001-877478	20010608
WO 2002081494	A1	20021017	WO 2002-US9187	20020326
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2003148985	A1	20030807	US 2002-310294	20021205

PRIORITY APPLN. INFO.:	US 1992-882712	B1 19920514
	US 1994-193627	A1 19940207
	US 1999-436430	A2 19991108
	US 2000-531025	B2 20000320
	US 2000-636385	B2 20000809
	US 2000-696347	B2 20001024
	US 2001-296876P	P 20010608
	US 2001-877478	B2 20010608
	US 2001-335059P	P 20011024
	US 2001-337055P	P 20011205
	US 2002-358580P	P 20020220
	US 2002-363124P	P 20020311

WO 2002-US9187	A2	20020326
US 2002-386782P	P	20020606
US 2002-406784P	P	20020829
US 2002-408378P	P	20020905
US 2002-409293P	P	20020909
AU 1995-26422	A3	19950518
US 1996-623891	A	19960325
AU 1996-76662	A3	19961025
US 2001-817879	A	20010326

AB The present invention concerns methods and reagents useful in modulating hepatitis B virus (HBV) gene expression in a variety of applications, including use in therapeutic, diagnostic, target validation, and genomic discovery applications. Specifically, the invention relates to short interfering nucleic acid (siNA) or short interfering RNA (siRNA sequenc) mols. capable of mediating RNA interference (RNAi) against against HBV polypeptide and polynucleotide targets. The instant invention also features various chemical modified synthetic short interfering RNA mols. capable of modulating HBV gene expression/activity in cells by RNA interference. Chemical modifications (2'-O-Me and 2'-deoxy-2'-fluoro groups in pyrimidine nucleotides, phosphorothioate linkages, 3'- and 5'-terminal caps comprising an inverted deoxy abasic moiety, etc.) in siRNA sequenc constructs are selected to yield nuclease resistance while preserving the ability to mediate RNAi activity. Exemplary siNA mols. are synthesized in tandem using standard phosphoramidite synthesis chemical and a cleavable linker, for example a succinyl-based linker, followed by a one-step purification process that provides RNAi mols. in high yield. The siNA mols. are designed that can bind to each target and are optionally individually analyzed by a computer folding algorithm to assess whether the siNA mol. can interact with the target sequence. The small interfering nucleic acid mols. are useful in the treatment and diagnosis of HBV infection, and any other condition that responds to modulation of HBV expression or activity.

IT **620691-28-3P 621022-88-6P 621022-90-0P 621022-91-1P**
RL: PAC (Pharmacological activity); PRP (Properties); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(siRNA; RNA interference-mediated inhibition of hepatitis B virus (HBV) gene expression using short interfering nucleic acid (siNA))

L2 ANSWER 11 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 07 Oct 2003
ACCESSION NUMBER: 2003:782588 CAPLUS
DOCUMENT NUMBER: 140:23855
TITLE: The Dog Genome: Survey sequencing and comparative analysis
AUTHOR(S): Kirkness, Ewen F.; Bafna, Vineet; Halpern, Aaron L.; Levy, Samuel; Remington, Karin; Rusch, Douglas

B.; Delcher, Arthur L.; Pop, Mihai; Wang, Wei; Fraser, Claire M.; Venter, J. Craig

CORPORATE SOURCE: The Institute for Genomic Research, Rockville, MD, 20850, USA

SOURCE: Science (Washington, DC, United States) (2003), 301(5641), 1898-1903
CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A survey of the dog genome sequence (6.22 million sequence reads; 1.5-fold coverage) demonstrates the power of sample sequencing for comparative anal. of mammalian genomes and the generation of species-specific resources. More than 650 million base pairs (>25%) of dog sequence align uniquely to the human genome, including fragments of putative orthologs for 18,473 of 24,567 annotated human genes. Mutation rates, conserved synteny, repeat content, and phylogeny can be compared among human, mouse, and dog. A variety of polymorphic elements are identified that will be valuable for mapping the genetic basis of diseases and traits in the dog. The genomic survey sequences are deposited in GenBank/EMBL/DDBJ under accession nos. CE000001-CE853796 and in the NCBI Genome Projects database under accession nos. AACN010000001-AACN011089636. [This abstract record is one of 214 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **599697-17-3**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; survey sequencing and comparative anal. of the dog genome)

L2 ANSWER 12 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN

ED Entered STN: 22 May 2002

ACCESSION NUMBER: 2002:379974 CAPLUS

DOCUMENT NUMBER: 136:381099

TITLE: The contribution of 700,000 ORF sequence tags to the definition of the human transcriptome

AUTHOR(S): Camargo, Anamaria A.; Samaia, Helena P. B.; Dias-Neto, Emmanuel; Simao, Daniel F.; Migotto, Italo A.; Briones, Marcelo R. S.; Costa, Fernando F.; Nagai, Maria Aparecida; Verjovski-Almeida, Sergio; Zago, Marco A.; Andrade, Luis Eduardo C.; Carrer, Helaine; El-Dorry, Hamza F. A.; Espreafico, Enilza M.; Habr-Gama, Angelita; Giannella-Neto, Daniel; Goldman, Gustavo H.; Gruber, Arthur; Hackel, Christine; Kimura, Edna T.; Maciel, Rui M. B.; Marie, Suely K. N.; Martins, Elizabeth A. L.; Nobrega, Marina P.; Paco-Larson, Maria Luisa; Pardini, Maria Ines M. C.; Pereira, Goncalo G.; Pesquero, Joao Bosco; Rodrigues, Vanderlei; Rogatto, Silvia R.; Da Silva, Ismael D. C. G.; Sogayar, Mari C.; Sonati, Maria De Fatima; Tajara, Eloiza H.; Valentini, Sandro R.; Alberto, Fernando L.; Amaral, Maria Elisabete J.; Aneas, Ivy; Arnaldi, Liliane A. T.; De Assis, Angela M.; Bengtson, Mario Henrique; Bergamo, Nadia Aparecida; Bombonato, Vanessa; De

Camargo, Maria E. R.; Canevari, Renata A.; Carraro, Dirce M.; Cerutti, Janete M.; Correa, Maria Lucia C.; Correa, Rosana F. R.; Costa, Maria Cristina R.; Curcio, Cyntia; Hokama, Paula O. M.; Ferreira, Ari J. S.; Furuzawa, Gilberto K.; Gushiken, Tsieko; Ho, Paulo L.; Kimura, Elza; Krieger, Jose E.; Leite, Luciana C. C.; Majumder, Paromita; Marins, Mozart; Marques, Everaldo R.; Melo, Analy S. A.; Barbosa de Melo, Monica; Mestriner, Carlos Alberto; Miracca, Elisabete C.; Miranda, Daniela C.; Nascimento, Ana Lucia T. O.; Nobrega, Francisco G.; Ojopi, Elida P. B.; Pandolfi, Jose Rodrigo C.; Pessoa, Luciana G.; Prevedel, Aline C.; Rahal, Paula; Rainho, Claudia A.; Reis, Eduardo M. R.; Ribeiro, Marcelo L.; Da Ros, Nancy; De Sa, Renata G.; Sales, Magaly M.; Sant'anna, Simone Cristina; Dos Santos, Mariana L.; Da Silva, Aline M.; Da Silva, Neusa P.; Silva, Wilson A., Jr.; Da Silveira, Rosana A.; Sousa, Josane F.; Stecconi, Daniella; Tsukumo, Fernando; Valente, Valeria; Soares, Fernando; Moreira, Eloisa S.; Nunes, Diana N.; Correa, Ricardo G.; Zalcberg, Heloisa; Carvalho, Alex F.; Reis, Luis F. L.; Brentani, Ricardo R.; Simpson, Andrew J. G.; De Souza, Sandro J.

CORPORATE SOURCE: Ludwig Institute for Cancer Research, Sao Paulo, 01509-010, Brazil

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2001), 98(21), 12103-12108
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Open reading frame expressed sequences tags (ORESTES) differ from conventional ESTs by providing sequence data from the central protein coding portion of transcripts. A total of 696,745 ORESTES sequences were generated from 24 human tissues and a subset of the data that correspond to a set of 15,095 full-length mRNAs used as a means of assessing the efficiency of the strategy and its potential contribution to the definition of the human transcriptome. It was estimated that ORESTES sampled over 80% of all highly and moderately expressed, and between 40% and 50% of rarely expressed, human genes. In the most thoroughly sequenced tissue, the breast, the 130,000 ORESTES generated are derived from transcripts from an estimated 70% of all genes expressed in that tissue, with an equally efficient representation of both highly and poorly expressed genes. In this respect, the capacity of the ORESTES strategy both for gene discovery and shotgun transcript sequence generation significantly exceeds that of conventional ESTs. The distribution of ORESTES is such that many human transcripts are now represented by a scaffold of partial sequences distributed along the length of each gene product. The exptl. joining of the scaffold components, by reverse transcription-PCR, represents a direct route to transcript finishing that may represent a useful alternative to full-length cDNA cloning. [This abstract record is one of 186 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **342460-43-9**, GenBank BI049449

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

L2 ANSWER 13 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 13 May 2002
ACCESSION NUMBER: 2002:354330 CAPLUS
DOCUMENT NUMBER: 136:364605
TITLE: The contribution of 700,000 ORF sequence tags to the definition of the human transcriptome
AUTHOR(S): Camargo, Anamaria A.; Samaia, Helena P. B.; Dias-Neto, Emmanuel; Simao, Daniel F.; Migotto, Italo A.; Briones, Marcelo R. S.; Costa, Fernando F.; Nagai, Maria Aparecida; Verjovski-Almeida, Sergio; Zago, Marco A.; Andrade, Luis Eduardo C.; Carrer, Helaine; El-Dorry, Hamza F. A.; Espreafico, Enilza M.; Habr-Gama, Angelita; Giannella-Neto, Daniel; Goldman, Gustavo H.; Gruber, Arthur; Hackel, Christine; Kimura, Edna T.; Maciel, Rui M. B.; Marie, Suely K. N.; Martins, Elizabeth A. L.; Nobrega, Marina P.; Paco-Larson, Maria Luisa; Pardini, Maria Ines M. C.; Pereira, Goncalo G.; Pesquero, Joao Bosco; Rodrigues, Vanderlei; Rogatto, Silvia R.; Da Silva, Ismael D. C. G.; Sogayar, Mari C.; Sonati, Maria De Fatima; Tajara, Eloiza H.; Valentini, Sandro R.; Alberto, Fernando L.; Amaral, Maria Elisabete J.; Aneas, Ivy; Arnaldi, Liliane A. T.; De Assis, Angela M.; Bengtson, Mario Henrique; Bergamo, Nadia Aparecida; Bombonato, Vanessa; De Camargo, Maria E. R.; Canevari, Renata A.; Carraro, Dirce M.; Cerutti, Janete M.; Correa, Maria Lucia C.; Correa, Rosana F. R.; Costa, Maria Cristina R.; Curcio, Cyntia; Hokama, Paula O. M.; Ferreira, Ari J. S.; Furuzawa, Gilberto K.; Gushiken, Tsieko; Ho, Paulo L.; Kimura, Elza; Krieger, Jose E.; Leite, Luciana C. C.; Majumder, Paromita; Marins, Mozart; Marques, Everaldo R.; Melo, Analy S. A.; Barbosa de Melo, Monica; Mestriner, Carlos Alberto; Miracca, Elisabete C.; Miranda, Daniela C.; Nascimento, Ana Lucia T. O.; Nobrega, Francisco G.; Ojopi, Elida P. B.; Pandolfi, Jose Rodrigo C.; Pessoa, Luciana G.; Prevedel, Aline C.; Rahal, Paula; Rainho, Claudia A.; Reis, Eduardo M. R.; Ribeiro, Marcelo L.; Da Ros, Nancy; De Sa, Renata G.; Sales, Magaly M.; Sant'anna, Simone Cristina; Dos Santos, Mariana L.; Da Silva, Aline M.; Da Silva, Neusa P.; Silva, Wilson A., Jr.; Da Silveira, Rosana A.; Sousa, Josane F.; Stecconi, Daniella; Tsukumo, Fernando; Valente, Valeria; Soares, Fernando; Moreira, Eloisa S.; Nunes, Diana N.; Correa, Ricardo G.; Zalcberg, Heloisa; Carvalho, Alex F.; Reis, Luis F. L.; Brentani, Ricardo R.; Simpson, Andrew J. G.; De Souza, Sandro J.
CORPORATE SOURCE: Ludwig Institute for Cancer Research, Sao Paulo, 01509-010, Brazil
SOURCE: Proceedings of the National Academy of Sciences of

the United States of America (2001), 98(21), 12103-12108
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Open reading frame expressed sequences tags (ORESTES) differ from conventional ESTs by providing sequence data from the central protein coding portion of transcripts. A total of 696,745 ORESTES sequences were generated from 24 human tissues and a subset of the data that correspond to a set of 15,095 full-length mRNAs used as a means of assessing the efficiency of the strategy and its potential contribution to the definition of the human transcriptome. It was estimated that ORESTES sampled over 80% of all highly and moderately expressed, and between 40% and 50% of rarely expressed, human genes. In the most thoroughly sequenced tissue, the breast, the 130,000 ORESTES generated are derived from transcripts from an estimated 70% of all genes expressed in that tissue, with an equally efficient representation of both highly and poorly expressed genes. In this respect, the capacity of the ORESTES strategy both for gene discovery and shotgun transcript sequence generation significantly exceeds that of conventional ESTs. The distribution of ORESTES is such that many human transcripts are now represented by a scaffold of partial sequences distributed along the length of each gene product. The exptl. joining of the scaffold components, by reverse transcription-PCR, represents a direct route to transcript finishing that may represent a useful alternative to full-length cDNA cloning. [This abstract record is one of 186 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **305138-76-5**, GenBank BF327943
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

L2 ANSWER 14 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 05 May 2002
ACCESSION NUMBER: 2002:332793 CAPLUS
DOCUMENT NUMBER: 136:351172
TITLE: The contribution of 700,000 ORF sequence tags to the definition of the human transcriptome
AUTHOR(S): Camargo, Anamaria A.; Samaia, Helena P. B.; Dias-Neto, Emmanuel; Simao, Daniel F.; Migotto, Italo A.; Briones, Marcelo R. S.; Costa, Fernando F.; Nagai, Maria Aparecida; Verjovski-Almeida, Sergio; Zago, Marco A.; Andrade, Luis Eduardo C.; Carrer, Helaine; El-Dorry, Hamza F. A.; Espreafico, Enilza M.; Habr-Gama, Angelita; Giannella-Neto, Daniel; Goldman, Gustavo H.; Gruber, Arthur; Hackel, Christine; Kimura, Edna T.; Maciel, Rui M. B.; Marie, Suely K. N.; Martins, Elizabeth A. L.; Nobrega, Marina P.; Paco-Larson, Maria Luisa; Pardini, Maria Ines M. C.; Pereira, Goncalo G.; Pesquero, Joao Bosco; Rodrigues, Vanderlei; Rogatto, Silvia R.; Da Silva, Ismael D. C. G.; Sogayar, Mari C.; Sonati, Maria De Fatima; Tajara, Eloiza H.; Valentini, Sandro R.; Alberto, Fernando L.; Amaral, Maria

Elisabete J.; Aneas, Ivy; Arnaldi, Liliane A. T.; De Assis, Angela M.; Bengtson, Mario Henrique; Bergamo, Nadia Aparecida; Bombonato, Vanessa; De Camargo, Maria E. R.; Canevari, Renata A.; Carraro, Dirce M.; Cerutti, Janete M.; Correa, Maria Lucia C.; Correa, Rosana F. R.; Costa, Maria Cristina R.; Curcio, Cyntia; Hokama, Paula O. M.; Ferreira, Ari J. S.; Furuzawa, Gilberto K.; Gushiken, Tsieko; Ho, Paulo L.; Kimura, Elza; Krieger, Jose E.; Leite, Luciana C. C.; Majumder, Paromita; Marins, Mozart; Marques, Everaldo R.; Melo, Analy S. A.; Barbosa de Melo, Monica; Mestriner, Carlos Alberto; Miracca, Elisabete C.; Miranda, Daniela C.; Nascimento, Ana Lucia T. O.; Nobrega, Francisco G.; Ojopi, Elida P. B.; Pandolfi, Jose Rodrigo C.; Pessoa, Luciana G.; Prevedel, Aline C.; Rahal, Paula; Rainho, Claudia A.; Reis, Eduardo M. R.; Ribeiro, Marcelo L.; Da Ros, Nancy; De Sa, Renata G.; Sales, Magaly M.; Sant'anna, Simone Cristina; Dos Santos, Mariana L.; Da Silva, Aline M.; Da Silva, Neusa P.; Silva, Wilson A., Jr.; Da Silveira, Rosana A.; Sousa, Josane F.; Stecconi, Daniella; Tsukumo, Fernando; Valente, Valeria; Soares, Fernando; Moreira, Eloisa S.; Nunes, Diana N.; Correa, Ricardo G.; Zalcberg, Heloisa; Carvalho, Alex F.; Reis, Luis F. L.; Brentani, Ricardo R.; Simpson, Andrew J. G.; De Souza, Sandro J.

CORPORATE SOURCE: Ludwig Institute for Cancer Research, Sao Paulo, 01509-010, Brazil

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2001), 98(21), 12103-12108
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Open reading frame expressed sequences tags (ORESTES) differ from conventional ESTs by providing sequence data from the central protein coding portion of transcripts. A total of 696,745 ORESTES sequences were generated from 24 human tissues and a subset of the data that correspond to a set of 15,095 full-length mRNAs used as a means of assessing the efficiency of the strategy and its potential contribution to the definition of the human transcriptome. It was estimated that ORESTES sampled over 80% of all highly and moderately expressed, and between 40% and 50% of rarely expressed, human genes. In the most thoroughly sequenced tissue, the breast, the 130,000 ORESTES generated are derived from transcripts from an estimated 70% of all genes expressed in that tissue, with an equally efficient representation of both highly and poorly expressed genes. In this respect, the capacity of the ORESTES strategy both for gene discovery and shotgun transcript sequence generation significantly exceeds that of conventional ESTs. The distribution of ORESTES is such that many human transcripts are now represented by a scaffold of partial sequences distributed along the length of each gene product. The exptl. joining of the scaffold components, by reverse transcription-PCR, represents a direct route to transcript finishing that may represent a useful alternative to full-length cDNA cloning. [This abstract record is one of 186 records for this document

necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **274053-54-2**, GenBank BE144757
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

L2 ANSWER 15 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 12 Apr 2002
ACCESSION NUMBER: 2002:276018 CAPLUS
DOCUMENT NUMBER: 136:320376
TITLE: Listeria innocua and Listeria monocytogenes genomic sequences and their applications
INVENTOR(S): Kunst, Frederik; Glaser, Philippe
PATENT ASSIGNEE(S): Institut Pasteur, Fr.; Centre National de la Recherche Scientifique (CNRS)
SOURCE: PCT Int. Appl., 180 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: French
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002028891	A2	20020411	WO 2001-FR3061	20011004
WO 2002028891	A3	20030103		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
FR 2814754	A1	20020405	FR 2000-12697	20001004
CA 2424952	AA	20020411	CA 2001-2424952	20011004
AU 2002014081	A5	20020415	AU 2002-14081	20011004
EP 1322763	A2	20030702	EP 2001-982519	20011004
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
JP 2004515227	T2	20040527	JP 2002-532473	20011004
US 2004018514	A1	20040129	US 2003-398221	20030710
PRIORITY APPLN. INFO.:			FR 2000-12697 A	20001004
			WO 2001-FR3061 W	20011004

AB The invention concerns nucleotide sequences derived from the genomes of Listeria innocua strain CLIP 11262 and Listeria monocytogenes strain 4b (CLIP 80459) and EGDe. Comparisons of the genomes identified genes specific to L. innocua (not found in L. monocytogenes) or specific to L. monocytogenes (not found in L. innocua). The sequences have application in the production of protein products by cloning, screening for modulators of gene expression to prevent Listeria or other bacterial infections in animal or human

hosts, the development of vaccines, and in the development of nucleic acid-based or antibody-based assays for Listeria genes and proteins.

IT **412391-99-2**
RL: ANT (Analyte); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; Listeria innocua and Listeria monocytogenes genomic sequences and their applications)

L2 ANSWER 16 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 11 Mar 2002
ACCESSION NUMBER: 2002:173233 CAPLUS
DOCUMENT NUMBER: 136:396927
TITLE: Reagents and kits, such as nucleic acid arrays, for detecting the expression of over 10,000 Drosophila genes
INVENTOR(S): Venter, J. Craig; Adams, Mark; Li, Peter W. D.; Myers, Eugene W.
PATENT ASSIGNEE(S): PE Corporation (NY), USA
SOURCE: PCT Int. Appl., 21 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 10
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001071042	A2	20010927	WO 2001-XB9231	20010323
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
WO 2001071042	A2	20010927	WO 2001-US9231	20010323
WO 2001071042	A3	20030313		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.:	US 2000-191637P	P	20000323
	US 2000-614150	A	20000711
	WO 2001-US9231	A	20010323

AB The present invention is based on the sequencing and assembly of the Drosophila melanogaster genome. The present invention provides the

primary nucleotide sequence of a large portion of the Drosophila melanogaster genome in a series of genomic and predicted transcript sequences. This information is provided in the form of genomic, transcript and protein sequence information and can be used to generate nucleic acid detection reagents and kits such as nucleic acid arrays. Primary sequences are provided as contiguous strings in a computer-readable format and recorded on media such as floppy disks, hard disks, magnetic tape, CD-ROM, RAM, ROM and hybrids of these categories. Genes/exons can be predicted, sequences can be edited and homol. searches of target motifs can be conducted. [This abstract record is one of ten records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **431371-50-5**
RL: ANT (Analyte); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; reagents and kits, such as nucleic acid arrays, for detecting the expression of over 10,000 Drosophila genes)

L2 ANSWER 17 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 30 Oct 2001
ACCESSION NUMBER: 2001:785622 CAPLUS
DOCUMENT NUMBER: 135:314495
TITLE: Differentially expressed nucleic acids encoding tumor-associated proteins, kits, and methods for identification, assessment, prevention, and therapy of human prostate cancer
INVENTOR(S): Schlegel, Robert; Endege, Wilson; Monahan, John E.
PATENT ASSIGNEE(S): Millennium Predictive Medicine, Inc., USA
SOURCE: PCT Int. Appl., 975 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001053836	A2	20010726	WO 2001-XC2318	20010124
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
WO 2001053836	A2	20010726	WO 2001-US2318	20010124
WO 2001053836	A3	20020606		
WO 2001053836	C2	20021107		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:

US 2000-178525P	P	20000124
US 2000-183245P	P	20000217
US 2000-190139P	P	20000316
US 2000-208126P	P	20000531
US 2000-219705P	P	20000718
US 2000-255160P	P	20001213
WO 2001-US2318	A	20010124

AB This invention relates to newly discovered correlations between expression of certain nucleic acid markers and the cancerous state of human prostate cells. The levels of expression of individual markers and combinations of markers described herein correlates with the presence of prostate cancer or a pre-malignant condition in a patient. Methods are provided for detecting the presence of prostate cancer in a sample, the absence of prostate cancer in a sample, the stage of a prostate cancer, the metastatic potential of a prostate cancer, the indolence or aggressiveness of the cancer, and other characteristics of prostate cancer that are relevant to prevention, diagnosis, characterization and therapy of prostate cancer in a patient. Thousands of differentially-expressed cDNA markers are identified in subtracted cDNA libraries and by transcript profiling. [This abstract record is the fourth of four records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **200320-90-7**
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; differentially expressed nucleic acids encoding tumor-associated proteins, kits, and methods for identification, assessment, prevention, and therapy of human prostate cancer)

L2 ANSWER 18 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 11 Apr 2001
ACCESSION NUMBER: 2001:255245 CAPLUS
DOCUMENT NUMBER: 134:265146
TITLE: Cloning and characterization of outer membrane protein OMP106 gene of Moraxella catarrhalis and its prophylactic, diagnostic and therapeutic uses
INVENTOR(S): Tucker, Kenneth; Plosila, Laura; Tillman, Ulrich F.
PATENT ASSIGNEE(S): Antex Biologics Inc., USA
SOURCE: U.S., 49 pp., Cont.-in-part of U.S. Ser. No. 642,712.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6214981	B1	20010410	US 1997-968685	19971112
CN 1223549	A	19990721	CN 1997-195990	19970428
ES 2202624	T3	20040401	ES 1997-926409	19970428
TW 541314	B	20030711	TW 1997-86105809	19970501
ZA 9703809	A	19971201	ZA 1997-3809	19970502
KR 2000010734	A	20000225	KR 1998-708845	19981103
US 2002177200	A1	20021128	US 2001-813214	20010320
PRIORITY APPLN. INFO.:			US 1996-642712 A2	19960503
			US 1997-968685 A3	19971112

AB The invention discloses the Moraxella catarrhalis outer membrane protein-106 (OMP106) polypeptide, polypeptides derived therefrom (OMP106-derived polypeptides), nucleotide sequences encoding these polypeptides, and antibodies that specifically bind the OMP106 polypeptide and/or OMP106-derived polypeptides. Also disclosed are immunogenic, prophylactic or therapeutic compns., including vaccines, comprising OMP106 polypeptide and/or OMP106-derived polypeptides. The invention addnl. discloses methods of inducing immune responses to M. catarrhalis and M. catarrhalis OMP106 polypeptides and OMP106-derived polypeptides in animals.

IT **332002-96-7 332002-97-8**
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; cloning and characterization of outer membrane protein OMP106 gene of Moraxella catarrhalis and its prophylactic, diagnostic and therapeutic uses)

REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 19 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 29 Mar 2001
ACCESSION NUMBER: 2001:224133 CAPLUS
DOCUMENT NUMBER: 135:353381
TITLE: Genotype-specific analysis of hepatitis B virus DNA on the LightCycler
AUTHOR(S): Sommer, Gunhild; Will, Hans
CORPORATE SOURCE: Heinrich-Pette-Institut fur Experimentelle Virologie und Immunologie, Universitat Hamburg, Hamburg, 20251, Germany
SOURCE: Rapid Cycle Real-Time PCR (2001), 303-311. Editor(s): Meuer, Stefan; Wittwer, Carl; Nakagawara, Kan-ichi. Springer-Verlag: Berlin, Germany.
CODEN: 69BBXY
DOCUMENT TYPE: Conference
LANGUAGE: English

AB The authors present a reproducible and sensitive method for quantification of hepatitis B virus (HBV)-DNA from specific genotypes by real-time polymerase chain reaction (PCR) on LightCycler which can be conducted in less than 2 h, including sample preparation, PCR, and data evaluation. This method may help to answer open questions regarding mechanisms involved in the viral life cycle, virus infection, hepatopathogenesis, and antiviral treatment.

IT **372211-31-9D**, 3'-fluorescein
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(probe; genotype-specific anal. of hepatitis B virus DNA on LightCycler)
REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 20 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 02 Feb 2001
ACCESSION NUMBER: 2001:78537 CAPLUS
DOCUMENT NUMBER: 134:144470
TITLE: A high molecular weight major outer membrane protein of Moraxella and the gene encoding it and the diagnosis, prophylaxis and treatment of infection
INVENTOR(S): Loosmore, Sheena M.; Sasaki, Ken; Yang, Yan-Ping; Klein, Michel H.
PATENT ASSIGNEE(S): Connaught Laboratories Limited, Can.
SOURCE: PCT Int. Appl., 247 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001007619	A1	20010201	WO 2000-CA870	20000726
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2379400	AA	20010201	CA 2000-2379400	20000726
EP 1203082	A1	20020508	EP 2000-951136	20000726
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				
NZ 517235	A	20040130	NZ 2000-517235	20000726
AU 774840	B2	20040708	AU 2000-64187	20000726
NZ 527727	A	20040730	NZ 2000-527727	20000726
NZ 527726	A	20040827	NZ 2000-527726	20000726
PRIORITY APPLN. INFO.:			US 1999-361619	A2 19990727
			NZ 2000-517235	A1 20000726
			WO 2000-CA870	W 20000726

AB An isolated and purified outer membrane protein of a Moraxella strain, particularly M. catarrhalis, having a mol. mass of about 200 kDa, is provided by recombinant means. The about 200 kDa outer membrane protein as well as nucleic acid mols. encoding the same are useful in diagnostic applications and immunogenic compns., particularly for in

vivo administration to a host to confer protection against disease caused by a bacterial pathogen that produces the about 200 kDa outer membrane protein or produces a protein capable of inducing antibodies in a host specifically reactive with the about 200 kDa outer membrane protein. N-terminally and C-terminally truncated about 200 kDa proteins also are produced recombinantly. The gene was cloned from the 4223 strain by screening an expression library in λEMBL3 with antiserum to the protein. A series of overlapping fragments were obtained and assembled to give the full-length gene. The gene was then used as a probe to obtain the gene from a number of different strains of the bacterium. Protein manufactured in Escherichia coli was obtained as inclusion bodies that could be resolubilized and used raise antiserum in mice and guinea pigs. The antiserum was bactericidal and could block the binding of the bacterium to animal cells. Comparison of the sequences of the G tract of genes from strains with different clumping activity indicated that the number of G's in the tract affected levels of gene expression. Preparation and characterization of N- and C-terminal truncation derivs. is described.

IT **323218-42-4**
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; high mol. weight major outer membrane protein of Moraxella and gene encoding it and diagnosis, prophylaxis and treatment of infection)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 21 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 18 Apr 2000
ACCESSION NUMBER: 2000:246921 CAPLUS
DOCUMENT NUMBER: 132:275067
TITLE: The genome sequence of Drosophila melanogaster
AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Phillipe; Burtis, Kenneth C.; Busam, Dana A.; Butler, Heather; Cadieu, Edouard; Center, Angela; Chandra, Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke, Carl; Davenport, Lionel B.; Davies, Peter; De Pablos, Beatriz; Delcher, Arthur; Deng, Zuoming; Mays, Anne Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson,

Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha, Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin, Kenneth J.; Evangelista, Carlos C.; Ferraz, Concepcion; Ferriera, Steven; Fleischmann, Wolfgang; Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.; Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong, Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan, Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon; Heiman, Thomas J.; Hernandez, Judith R.; Houck, Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland, Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali, Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi; Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz, Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei, Yiding; Levitsky, Alexander A.; Li, Jiayin; Li, Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun; Mattei, Bettina; McIntosh, Tina C.; McLeod, Michael P.; McPherson, Duncan; Merkulov, Gennady; Milshina, Natalia V.; Mobarry, Clark; Morris, Joe; Moshrefi, Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian; Murphy, Lee; Muzny, Donna M.; Nelson, David L.; Nelson, David R.; Nelson, Keith A.; Nixon, Katherine; Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo, Michael; Pittman, Gjange S.; Pan, Sue; Pollard, John; Puri, Vinita; Reese, Martin G.; Reinert, Knut; Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; Shen, Hua; Shue, Bixiang Christopher; Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.; Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas, Robert; Tector, Cyndee; Turner, Russell; Venter, Eli; Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman, David A.; Weinstock, George M.; Weissenbach, Jean; Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.; Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh, Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang, Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu, Shiaoping; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs, Richard A.; Myers, Eugene W.; Rubin, Gerald M.; Venter, J. Craig

CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA

SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195
CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The fly Drosophila melanogaster is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was determined of nearly all of the .apprx.120-megabase euchromatic portion of the Drosophila genome using a whole-genome shotgun sequencing strategy

supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller Caenorhabditis elegans genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at http://flybase.bio.indiana.edu and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstract record is one of 4 records for this document necessitated by the large number of index entries required to fully index the document and publication system restraints.].

IT **260229-53-6**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; genome sequence of Drosophila melanogaster)

L2 ANSWER 22 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 03 Apr 1998
ACCESSION NUMBER: 1998:194986 CAPLUS
DOCUMENT NUMBER: 128:226228
TITLE: Antiviral oligonucleotides interfering with the replication of hepatitis B virus and their therapeutic use
INVENTOR(S): Carmichael, Ellen
PATENT ASSIGNEE(S): Immune Response Corp., USA
SOURCE: U.S., 14 pp., Cont.-in-part of U.S. Ser. No. 181,557, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5728518	A	19980317	US 1994-287337	19940808
CA 2180347	AA	19950720	CA 1995-2180347	19950111
WO 9519433	A2	19950720	WO 1995-US508	19950111
WO 9519433	A3	19951019		
W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SI, SK, TJ, TT, UA, UZ				
RW: KE, MW, SD, SZ, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9516800	A1	19950801	AU 1995-16800	19950111
AU 704562	B2	19990429		
EP 739415	A1	19961030	EP 1995-908507	19950111
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 09511382	T2	19971118	JP 1995-519146	19950111
PRIORITY APPLN. INFO.:			US 1994-181557 B2	19940112
			US 1994-287337 A	19940808

WO 1995-US508 W 19950111

AB Oligonucleotides that inhibit viral replication, particularly hepatitis virus replication, such as hepatitis B virus (HBV) replication, are described for use as antivirals. Preferred hepatitis B virus targets for these oligonucleotides include RNA primer binding regions such as the DRII region, the transcript of the viral DNA polymerase gene or transcripts of envelope or surface protein genes such as the pre-S1 protein involved in cell attachment, or the viral cis-encapsidation signal. These oligonucleotides can be used for detection of the presence of viral nucleic acid, particularly HBV DNA, in a cell and can be used to treat viral infection. Oligonucleotides directed against these targets inhibited viral replication in vitro with IC50s in the range 4-20 μM. When these oligonucleotides were delivered as a complex with a polylysine-orosomucoid conjugate, then the IC50s fell to 1-5 μM.

IT **168119-01-5**
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; antiviral oligonucleotides interfering with replication of hepatitis B virus and their therapeutic use)

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 23 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 13 Nov 1997
ACCESSION NUMBER: 1997:718044 CAPLUS
DOCUMENT NUMBER: 128:19356
TITLE: Line probe assay [LiPA test strip] for genotyping and detecting HBV in blood serum
INVENTOR(S): Stuyver, Lieven; Rossau, Rudi; Maertens, Geert
PATENT ASSIGNEE(S): Innogenetics N.V., Belg.; Stuyver, Lieven; Rossau, Rudi; Maertens, Geert
SOURCE: PCT Int. Appl., 80 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9740193	A2	19971030	WO 1997-EP2002	19970421
WO 9740193	A3	19980507		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
ZA 9703367	A	19971118	ZA 1997-3367	19970418
AU 9727662	A1	19971112	AU 1997-27662	19970421
EP 914472	A2	19990512	EP 1997-921677	19970421
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
US 6709812	B1	20040323	US 1998-155885	19981008

US 2004029110 A1 20040212 US 2003-453792 20030604
PRIORITY APPLN. INFO.: EP 1996-870053 A 19960419
WO 1997-EP2002 W 19970421
US 1998-155885 A3 19981008

AB A method for detection and/or genetic anal. of one or more hepatitis B virus in a biol. sample is described. It relates hybridizing the nucleic acids of the sample with a combination of at least two nucleotide probes targeting mutant sequence chosen from the HBV RT pol gene region and/or the HBV preCore region and/or to mutant HBsAg region HBV genotype-specific target sequence. The probes are associated with a solid support and are capable of hybridizing to the polynucleic acids of the sample under the same hybridization and wash conditions. The HBV genotype and/or mutants present in said sample is inferred from the differential hybridization signal(s) obtained. Sets of nucleotide probes and primers useful for typing and/or detecting HBV using assay kits are described.

IT **199198-12-4**
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence of HBPr41; line Probe Assay [LiPA test strip] for genotyping and detecting HBV in blood serum)

IT **199198-20-4**
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence of HBPr48; line Probe Assay [LiPA test strip] for genotyping and detecting HBV in blood serum)

L2 ANSWER 24 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 29 Sep 1997
ACCESSION NUMBER: 1997:620064 CAPLUS
DOCUMENT NUMBER: 127:303740
TITLE: Colorimetric point mutation assay: for detection of precore mutants of hepatitis B
AUTHOR(S): Ballard, A. L.; Boxall, E. H.
CORPORATE SOURCE: Public Health Lab., Birmingham Heartlands and Solihull NHS Trust, Heartlands Hosp., Birmingham, B9 5SS, UK
SOURCE: Journal of Virological Methods (1997), 67(2), 143-152
CODEN: JVMEDH; ISSN: 0166-0934
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A colorimetric assay for the anal. of point mutations in PCR-amplified DNA fragments from hepatitis B virus (HBV) is described. The method was applied for anal. of the single point mutation in codon 28 of the precore gene of HBV, which inhibits expression of HBe antigen. The assay, which uses a microtiter plate format, incorporates fluorescein-labeled dideoxynucleotides as opposed to radioactively-labeled deoxynucleotides used in methods described previously. Synthetic control wild-type and mutant oligonucleotides were tested to optimize the reaction conditions. The assay was thus shown to yield both qual. and quant. data on the relative proportions of wild-type and mutant sequences within a given sample. Amplicons

from clin. specimens of known sequence were analyzed to validate the assay. Sixteen chronic carriers of HBV were tested using the codon 28 point mutation assay, and the results were confirmed by directing sequencing. The method described is suitable for applications where point mutations are of interest.

IT **197253-19-3**, DNA (synthetic primer Bio-MT)
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses) (control primer Bio-MT; colorimetric point mutation assay for detection of precore mutants of hepatitis B)

IT **197253-18-2**, DNA (synthetic primer Bio-WT)
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses) (control primer Bio-WT; colorimetric point mutation assay for detection of precore mutants of hepatitis B)

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 25 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 22 Mar 1997
ACCESSION NUMBER: 1997:189990 CAPLUS
DOCUMENT NUMBER: 126:181341
TITLE: Antisense inhibition of hepatitis B virus replication
INVENTOR(S): Anderson, Kevin P.; Cowsert, Lex M.
PATENT ASSIGNEE(S): Isis Pharmaceuticals, Inc., USA; Anderson, Kevin P.; Cowsert, Lex M.
SOURCE: PCT Int. Appl., 45 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9703211	A1	19970130	WO 1996-US10984	19960626
W: AL, AM, AU, BB, BG, BR, CA, CN, CZ, EE, FI, GE, HU, IL, IS, JP, KG, KP, KR, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, SG, SI, SK, TR, TT, UA, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 5985662	A	19991116	US 1995-501968	19950713
CA 2223645	AA	19970130	CA 1996-2223645	19960626
AU 9664796	A1	19970210	AU 1996-64796	19960626
EP 837951	A1	19980429	EP 1996-924309	19960626
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 10510435	T2	19981013	JP 1996-505848	19960626

PRIORITY APPLN. INFO.:
US 1995-501968 A 19950713
WO 1996-US10984 W 19960626

AB Antisense oligonucleotides are provided which are capable of inhibiting hepatitis B virus (HBV) replication. These oligonucleotides are specifically hybridizable with HBV RNAs which encode a P gene product, S gene product or C gene product, or with the 5' cap region, U5 region, ε region, or translocation

initiation site of HBV RNA. Among the 40 antisense phosphorothioate oligodeoxyribonucleotides tested to date, 14 have EC90's below 10 μM and are presently preferred. Methods of diagnosing HBV infection, methods of inhibiting HBV replication, methods of treating an HBV infection and methods of treating or preventing HBV-associated diseases using the oligonucleotides of the invention are also provided. Such diseases may include acute hepatitis, chronic hepatitis, fulminant hepatitis, or hepatocellular carcinoma.

IT **187288-75-1 187288-85-3**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense inhibition of hepatitis B virus replication)

L2 ANSWER 26 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 06 Mar 1997
ACCESSION NUMBER: 1997:145211 CAPLUS
DOCUMENT NUMBER: 126:140560
TITLE: Method for detecting nucleic acid sequences using competitive amplification
INVENTOR(S): Birkenmeyer, Larry; Mushahwar, Isa K.
PATENT ASSIGNEE(S): Abbott Laboratories, USA
SOURCE: PCT Int. Appl., 39 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
WO 9640996	A1	19961219	WO 1996-US8429		19960603
W: CA, JP					
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE					
US 5667974	A	19970916	US 1995-480220		19950607
CA 2223823	AA	19961219	CA 1996-2223823		19960603
EP 832281	A1	19980401	EP 1996-917000		19960603
EP 832281	B1	20020109			
R: AT, BE, CH, DE, ES, FR, GB, IT, LI, NL					
JP 11506613	T2	19990615	JP 1996-501035		19960603
AT 211771	E	20020115	AT 1996-917000		19960603
ES 2171679	T3	20020916	ES 1996-917000		19960603
US 5955598	A	19990921	US 1997-864404		19970528
PRIORITY APPLN. INFO.:			US 1995-480220	A	19950607
			WO 1996-US8429	W	19960603

AB A method is provided for quant. detecting the amount of a target nucleic acid sequence which may be present in a test sample. A test sample which may contain a target nucleic acid sequence comprising target sequences X and Y is contacted with 2 primer sets, the first set being specific for target X and the second set being specific for target Y. The test sample also is contacted at the same time with an internal standard sequence IS, which is substantially derived from a combination of the first and second target sequences, and its corresponding oligonucleotide primer sets. Haptens are associated with the oligonucleotide primer sets in such a way that amplified target sequence products X and Y are detected by capture on a solid phase to which anti-hapten

capture reagents are attached. A signal ratio of (X + Y)/S is determined to quantitate the amount of the target nucleic acid sequence contained in the sample. The technique is applied to the quant. determination by gap ligase chain reaction (GLCR) of the DNA of hepatitis B virus, and primer sets are provided for (1) map positions 180-225 and 658-703 within the HBV genome, (2) distinguishing the wild-type and mutant codon 145 of the HBV S-gene, and (3) distinguishing the wild-type and mutant codon 28 of the HBV precore antigen gene.

IT **186675-93-4D**, 3'-fluorescein-labeled
RL: ANT (Analyte); ANST (Analytical study)
(primer for hepatitis B pre-core antigen gene codon 28; method for detecting nucleic acid sequences using competitive amplification)

L2 ANSWER 27 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 18 May 1996
ACCESSION NUMBER: 1996:298302 CAPLUS
DOCUMENT NUMBER: 124:333056
TITLE: Antisense oligonucleotides inhibiting replication of hepatitis B virus for treatment of chronic infection
INVENTOR(S): Korba, Brent E.; Gerin, John L.
PATENT ASSIGNEE(S): Georgetown University, USA
SOURCE: PCT Int. Appl., 55 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9603152	A1	19960208	WO 1995-US9143	19950728
W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TT				
RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 5646262	A	19970708	US 1994-281106	19940728
CA 2196070	AA	19960208	CA 1995-2196070	19950728
AU 9531024	A1	19960222	AU 1995-31024	19950728
AU 705132	B2	19990513		
EP 772454	A1	19970514	EP 1995-926752	19950728
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 10503367	T2	19980331	JP 1995-505846	19950728
US 6503533	B1	20030107	US 1998-199269	19981125

PRIORITY APPLN. INFO.:

US 1994-281106	A	19940728
WO 1995-US9143	W	19950728
US 1997-888695	B1	19970707

AB Antisense oligonucleotides that hybridize to segments of the preS1, S, C, and ε regions of the hepatitis B virus (HBV) RNA pregenome inhibit replication of the virus. Pharmaceutical compns. which contain these oligonucleotides as the active ingredients are effective against HBV infection. A panel of 56 phosphorothioate

oligonucleotides was tested in a cell culture assay for inhibition of viral replication.

IT **176635-15-7 176635-17-9 176709-86-7**
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide; antisense oligonucleotides inhibiting replication of hepatitis B virus for treatment of chronic infection)

L2 ANSWER 28 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 22 Dec 1995
ACCESSION NUMBER: 1995:996732 CAPLUS
DOCUMENT NUMBER: 124:78685
TITLE: Polypeptide derived from X region of variant hepatitis B virus, gene encoding the same, and use for diagnosis
INVENTOR(S): Uchida, Toshikazu; Shikata, Toshio
PATENT ASSIGNEE(S): Dainabot Co., Ltd., Japan
SOURCE: PCT Int. Appl., 61 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9527788	A1	19951019	WO 1995-JP700	19950410

W: JP, US
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
PRIORITY APPLN. INFO.: JP 1994-95458 A 19940411

AB Provided are a novel hepatitis B virus that cannot be detected by any of the type A, B, C, D and E virus tests and the cDNA of the variant X region. The cDNA of region X were isolated from patients E88 and H2 who showed acute and chronic hepatitis symptoms, but were neg. by the currently available tests. The polypeptide deduced from region X of clone E88 has 161 amino acid residues. The cDNA and the protein product can be used for diagnosis of hepatitis. The X protein as a product of X genes of the HBV is known to be not only useful as an antigen for detecting HBV infection but also capable of activating transcription by the trans-action thereof on the enhancer of the HBV itself or the enhancer of the promoter sequence of another cellular gene through the interaction with cell factors in normal liver cells. It may be used for the development of anti-viral and anti-tumor agents.

IT **172522-26-8**
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; cloning of cDNA of gene X of hepatitis B virus variant and its clin. applications)

IT **172522-28-0**
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; cloning of cDNA of gene X of hepatitis B virus variant and its use in diagnosis and treatment of diseases associated with)

L2 ANSWER 29 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN

ED Entered STN: 21 Sep 1995
ACCESSION NUMBER: 1995:804538 CAPLUS
DOCUMENT NUMBER: 123:218381
TITLE: Antiviral oligonucleotides interfering with the replication of hepatitis B virus and their therapeutic use
INVENTOR(S): Carmichael, Ellen
PATENT ASSIGNEE(S): Targetech, Inc., USA
SOURCE: PCT Int. Appl., 31 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9519433	A2	19950720	WO 1995-US508	19950111
WO 9519433	A3	19951019		
W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SI, SK, TJ, TT, UA, UZ				
RW: KE, MW, SD, SZ, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 5728518	A	19980317	US 1994-287337	19940808
AU 9516800	A1	19950801	AU 1995-16800	19950111
AU 704562	B2	19990429		
EP 739415	A1	19961030	EP 1995-908507	19950111
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 09511382	T2	19971118	JP 1995-519146	19950111
PRIORITY APPLN. INFO.:			US 1994-181557 A	19940112
			US 1994-287337 A	19940808
			WO 1995-US508 W	19950111

AB Oligonucleotides that inhibit viral replication, particularly hepatitis virus replication, such as hepatitis B virus (HBV) replication, are described for use as antivirals. Preferred hepatitis B virus targets for these oligonucleotides include RNA primer binding regions such as the DRII region, the transcript of the viral DNA polymerase gene or transcripts of envelope or surface protein genes such as the pre-S1 protein involved in cell attachment, or the viral cis-encapsidation signal. These oligonucleotides can be used for detection of the presence of viral nucleic acid, particularly HBV DNA, in a cell and can be used to treat viral infection. Oligonucleotides directed against these targets inhibited viral replication in vitro with IC50s in the range 4-20 μM. When these oligonucleotides were delivered as a complex with a polylysine-orosomucoid conjugate, then the IC50s fell to 1-5 μM.

IT **168119-01-5**
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; antiviral oligonucleotides interfering with replication of hepatitis B virus and their therapeutic use)

L2 ANSWER 30 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 13 Sep 1995
ACCESSION NUMBER: 1995:788986 CAPLUS
DOCUMENT NUMBER: 124:1994
TITLE: The hepatitis B virus X gene: analysis of functional domain variation and gene phylogeny using multiple sequences
AUTHOR(S): Kidd-Ljunggren, Karin; Oeberg, Monica; Kidd, Alistair H.
CORPORATE SOURCE: Dep. Infectious Diseases, Univ. Hosp. Lund, Lund, S-221 85, Swed.
SOURCE: Journal of General Virology (1995), 76(9), 2119-30
CODEN: JGVIAY; ISSN: 0022-1317
PUBLISHER: Society for General Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The hepatitis B virus (HBV) X gene shares sequences with both the polymerase and precore genes, carries several regulatory signals critical to the replicative cycle, and its product has a trans-activating function. In this study, the X gene sequences of 29 HBV strains from 14 different countries were characterized and compared to all corresponding databank sequences where the origin of the strain was stated. The X gene and its product are relatively well conserved. However, several rare or unique point mutations in the predicted X protein are described which further define regions on the primary sequence which may be of structural and/or functional significance. Phylogenetic anal. of the 29 X genes and their predicted proteins in this study using un-rooted trees indicates that a common ancestral sequence gave rise to two main groups of X genes, represented by HBV strains found predominantly either in the Western or Eastern hemisphere. In turn, each of these two main groups of sequences appear to have branched into two main lineage. Introduction of 33 addnl. DNA sequences from the databank has further verified these inferences and confirmed the groupings as previously described subgroups A to D. While the split of X gene lineages into subgroups A and D seems feasible on geog./anthropologica. grounds, the corresponding split of Eastern hemisphere lineages into B and C may require an alternative hypothesis. Addnl., there was a correlation between the HBeAg/anti-HBeAg status of our patients and nucleotide identity at two positions in the core promoter, 52 and 50 bases upstream from the precore start codon. This finding, also shown recently by others, suggests that control of HBeAg secretion may involve mutations affecting transcription and not only precore/core translation.
IT **148188-81-2**, GenBank V01460
RL: PRP (Properties)
(nucleotide sequence; anal. of functional domain variation and gene phylogeny using multiple sequences of hepatitis B virus X gene)

L2 ANSWER 31 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 26 May 1990
ACCESSION NUMBER: 1990:192774 CAPLUS
DOCUMENT NUMBER: 112:192774
TITLE: Studies on the structure of HBV DNA
AUTHOR(S): Qi, Zuhe; Yan, Jun; Zhu, Qinglin
CORPORATE SOURCE: Inst. Basic Med. Sci., Chin. Acad. Med. Sci., Beijing, 100730, Peop. Rep. China
SOURCE: Science in China, Series B: Chemistry, Life Sciences, & Earth Sciences (1989), 32(11), 1318-28

CODEN: SCBSE5; ISSN: 1001-652X
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The structure of hepatitis B virus adr NC-1 DNA was analyzed and compared with another 5 strains of HBV DNAs. Some of the prokaryotic promoter-like sequences, palindromic sequences, and ATAA are identified. An enhancer core sequence and some other characteristics are also shown. In considering the reading frame and its regulatory sequence as a transcriptional unit, some of the possible new frames are discussed.
IT **73247-02-6,** Deoxyribonucleic acid (hepatitis B virus subtype ayw)
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

L2 ANSWER 32 OF 32 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 12 May 1984
ACCESSION NUMBER: 1980:141944 CAPLUS
DOCUMENT NUMBER: 92:141944
TITLE: Nucleotide sequence of the hepatitis B virus genome (subtype ayw) cloned in E. coli
AUTHOR(S): Galibert, Francis; Mandart, Elisabeth; Fitoussi, Francoise; Tiollais, Pierre; Charnay, Patrick
CORPORATE SOURCE: Cent. Hayem, Hop. Saint-Louis, Paris, Fr.
SOURCE: Nature (London, United Kingdom) (1979), 281(5733), 646-50
CODEN: NATUAS; ISSN: 0028-0836
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The complete nucleotide sequence (3182 residues) of hepatitis B virus genome (subtype ayw) cloned in Escherichia coli was determined using the Maxam and Gilbert method and the dideoxynucleotide method. Location of the nonsense codons showed that the coding capacity of the L chain was larger than that of the S chain. Eight open regions, able to code for polypeptide chains >100 amino acids, were located, with the largest, region 6, covering >80% of the genome. The gene S, coding for polypeptide I of the hepatitis B antigen and previously located between coordinates 95.1 and 73.6, was contained in region 7.
IT **73247-02-6**
RL: PROC (Process)
(nucleotide sequence and coding anal. of)

E1 THROUGH E37 ASSIGNED

FILE 'REGISTRY' ENTERED AT 10:27:18 ON 05 APR 2005
L4 37 SEA FILE=REGISTRY ABB=ON PLU=ON (148188-81-2/BI OR 168119-01-5/BI OR 593230-84-3/BI OR 73247-02-6/BI OR 172522-26-8/BI OR 172522-28-0/BI OR 176635-15-7/BI OR 176635-17-9/BI OR 176709-86-7/BI OR 186675-93-4/BI OR 187288-75-1/BI OR 187288-85-3/BI OR 197253-18-2/BI OR 197253-19-3/BI OR 199198-12-4/BI OR 199198-20-4/BI OR 200320-90-7/BI OR 260229-53-6/BI OR 274053-54-2/BI OR 305138-76-5/BI OR 323218-42-4/BI OR 332002-96-7/BI OR 332002-97-8/BI OR 342460-43-9/BI OR 372211-31-9/BI OR 389735-54-0/BI OR 412391-99-2/BI OR 423908-16-1/BI OR 431371-50-5/BI OR 595461-40-8/BI OR 599697-17-3/BI OR 620691-28-3/BI OR 621022-88-6/BI OR 621022-90-0/BI OR 621022-91-1/BI OR 709063-06-9/BI OR 833920-72-2/BI)

L4 ANSWER 1 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **833920-72-2** REGISTRY
CN DNA (Gallus domesticus clone Ggal_76d_PR_G06 genome survey sequence) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank CL272028
SQL 250
MF Unspecified
CI MAN

REFERENCE 1: 142:170782

L4 ANSWER 2 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **709063-06-9** REGISTRY
CN DNA, d(C-C-T-A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A-C) (9CI) (CA INDEX NAME)
SQL 20
MF Unspecified
CI MAN

REFERENCE 1: 141:65785

L4 ANSWER 3 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **621022-91-1** REGISTRY
CN RNA, (C-A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A-C-A), complex with RNA (U-G-U-G-C-C-U-U-G-G-G-U-G-G-C-U-U-U-G) (1:1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 345: PN: US20030206887 SEQID: 577 claimed RNA
SQL 38,19,19
MF Unspecified
CI MAN

REFERENCE 1: 139:358726

L4 ANSWER 4 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **621022-90-0** REGISTRY
CN RNA, (C-C-C-A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A), complex with RNA (U-G-C-C-U-U-G-G-G-U-G-G-C-U-U-U-G-G-G) (1:1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 344: PN: US20030206887 SEQID: 576 claimed RNA
SQL 38,19,19
MF Unspecified
CI MAN

REFERENCE 1: 139:358726

L4 ANSWER 5 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **621022-88-6** REGISTRY
CN RNA, (C-C-A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A-C), complex with RNA (G-U-G-C-C-U-U-G-G-G-U-G-G-C-U-U-U-G-G) (1:1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 342: PN: US20030206887 SEQID: 574 claimed RNA
SQL 38,19,19
MF Unspecified
CI MAN

REFERENCE 1: 139:358726

L4 ANSWER 6 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **620691-28-3** REGISTRY

CN RNA, (A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A-C-A-G), complex with RNA (C-U-G-U-G-C-C-U-U-G-G-G-U-G-G-C-U-U-U) (1:1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 54: PN: US20030206887 SEQID: 54 claimed RNA
SQL 38,19,19
MF Unspecified
CI MAN

REFERENCE 1: 139:358726

L4 ANSWER 7 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **599697-17-3** REGISTRY
CN DNA (Canis familiaris strain Standard Poodle clone tigr-gss-dog-17000333941473 genome survey sequence) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank CE327035
SQL 441
MF Unspecified
CI MAN

REFERENCE 1: 140:23855

L4 ANSWER 8 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **595461-40-8** REGISTRY
CN DNA (Saccharum officinarum clone SCRLSB1042G03 EST (expressed sequence tag)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank CA192813
SQL 646
MF Unspecified
CI MAN

REFERENCE 1: 140:106239

L4 ANSWER 9 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **593230-84-3** REGISTRY
CN DNA (Saccharum officinarum clone SCEPAM2013G09 EST (expressed sequence tag)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank CA083440
SQL 666
MF Unspecified
CI MAN

REFERENCE 1: 140:88522

REFERENCE 2: 140:88521

L4 ANSWER 10 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **431371-50-5** REGISTRY
CN DNA (Drosophila melanogaster clone WO0171042-SEQID-9883 gene plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1381: PN: WO0171042 SEQID: 9883 claimed DNA
SQL 7085
MF Unspecified
CI MAN

REFERENCE 1: 136:396927

L4 ANSWER 11 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **423908-16-1** REGISTRY
CN DNA (Triticum aestivum clone WHE3092_F07_K14 EST (expressed sequence tag)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank BQ283554
SQL 540
MF Unspecified
CI MAN

REFERENCE 1: 142:18286

L4 ANSWER 12 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **412391-99-2** REGISTRY
CN DNA (Listeria monocytogenes strain CLIP80459 clone WO0228891-SEQID-3305 contig) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 3305: PN: WO0228891 SEQID: 3305 claimed DNA
SQL 1841
MF Unspecified
CI MAN

REFERENCE 1: 136:320376

L4 ANSWER 13 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **389735-54-0** REGISTRY
CN DNA (human cell line 5HL2-B clone R28194) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 219: PN: US20040009481 TABLE: 1 claimed DNA
CN GenBank AC003111
SQL 40649
MF Unspecified
CI MAN

REFERENCE 1: 140:123703

L4 ANSWER 14 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **372211-31-9** REGISTRY
CN DNA, d(C-C-A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A-C) (9CI) (CA INDEX NAME)
SQL 19
MF Unspecified
CI MAN

REFERENCE 1: 135:353381

L4 ANSWER 15 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **342460-43-9** REGISTRY
CN DNA (human clone CM2-GN0295-020101-655-a07 EST (expressed sequence tag)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank BI049449
SQL 396
MF Unspecified
CI MAN

REFERENCE 1: 136:381099

L4 ANSWER 16 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **332002-97-8** REGISTRY
CN DNA (Moraxella catarrhalis OMP (outer membrane protein) OMP106 gene) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 15: PN: US6214981 SEQID: 9 claimed DNA
SQL 6371
MF Unspecified
CI MAN

REFERENCE 1: 134:265146

L4 ANSWER 17 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **332002-96-7** REGISTRY
CN DNA (Moraxella catarrhalis OMP (outer membrane protein) OMP106 gene plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 6: PN: US6214981 SEQID: 9 claimed DNA
SQL 9542
MF Unspecified
CI MAN

REFERENCE 1: 134:265146

L4 ANSWER 18 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **323218-42-4** REGISTRY
CN DNA (Moraxella catarrhalis strain LES1 major outer membrane glycoprotein MOMP gene) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 6: PN: WO0107619 FIGURE: 5 claimed DNA
SQL 6942
MF Unspecified
CI MAN

REFERENCE 1: 134:144470

L4 ANSWER 19 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **305138-76-5** REGISTRY
CN DNA (human clone QV0-BN0148-070700-293-a12 EST (expressed sequence tag)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank BF327943
SQL 384
MF Unspecified
CI MAN

REFERENCE 1: 136:364605

L4 ANSWER 20 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **274053-54-2** REGISTRY
CN DNA (human clone CM0-HT0180-041099-065-c06 EST (expressed sequence tag)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank BE144757
SQL 496
MF Unspecified
CI MAN

REFERENCE 1: 136:351172

L4 ANSWER 21 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **260229-53-6** REGISTRY
CN DNA (Drosophila melanogaster genome scaffold 142000013386047 section 28 of 52) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AE002787
CN GenBank AE002787 (Secondary GenBank Accession Number)
CN GenBank AE003818
CN GenBank AE013599 (Secondary GenBank Accession Number)
SQL 291923
MF Unspecified
CI MAN

REFERENCE 1: 132:275067

L4 ANSWER 22 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **200320-90-7** REGISTRY
CN DNA (human cell line 5HL2-B clone R28194) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 109: PN: WO0153836 TABLE: 3-5 claimed DNA
SQL 40649
MF Unspecified
CI MAN

REFERENCE 1: 135:314495

L4 ANSWER 23 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **199198-20-4** REGISTRY
CN DNA, d(A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A-C-A) (9CI) (CA INDEX NAME)
SQL 18
MF Unspecified
CI MAN

REFERENCE 1: 128:19356

L4 ANSWER 24 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **199198-12-4** REGISTRY
CN DNA, d(A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A) (9CI) (CA INDEX NAME)
SQL 16
MF Unspecified
CI MAN

REFERENCE 1: 128:19356

L4 ANSWER 25 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **197253-19-3** REGISTRY
CN DNA (synthetic primer Bio-MT) (9CI) (CA INDEX NAME)
SQL 60
MF Unspecified
CI MAN

REFERENCE 1: 127:303740

L4 ANSWER 26 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **197253-18-2** REGISTRY
CN DNA (synthetic primer Bio-WT) (9CI) (CA INDEX NAME)
SQL 60
MF Unspecified

CI MAN

REFERENCE 1: 127:303740

L4 ANSWER 27 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **187288-85-3** REGISTRY
CN DNA, d(P-thio)(A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A-C-A-G-C) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(P-thio)(A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A-C-A-G-C)
OTHER NAMES:
CN Isis 9592
SQL 20
MF Unspecified
CI MAN

REFERENCE 1: 126:181341

L4 ANSWER 28 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **187288-75-1** REGISTRY
CN DNA, d(P-thio)(C-C-A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A-C-A-G) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(P-thio)(C-C-A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A-C-A-G)
OTHER NAMES:
CN Isis 5821
SQL 21
MF Unspecified
CI MAN

REFERENCE 1: 126:181341

L4 ANSWER 29 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **186675-93-4** REGISTRY
CN DNA, d(A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A-C-A), 5'-(dihydrogen phosphate) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A-C-A), 5'-(dihydrogen phosphate)
SQL 18
MF Unspecified
CI MAN

REFERENCE 1: 126:140560

L4 ANSWER 30 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **176709-86-7** REGISTRY
CN DNA, d(A-C-C-C-C-A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(A-C-C-C-C-A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A)
SQL 21
MF Unspecified
CI MAN

REFERENCE 1: 124:333056

L4 ANSWER 31 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **176635-17-9** REGISTRY
CN DNA, d(P-thio)(A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(P-thio)(A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A)
SQL 16
MF Unspecified
CI MAN

REFERENCE 1: 124:333056

L4 ANSWER 32 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **176635-15-7** REGISTRY
CN DNA, d(P-thio)(A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A-C-A-G-C-T) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(P-thio)(A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A-C-A-G-C-T)
SQL 21
MF Unspecified
CI MAN

REFERENCE 1: 124:333056

L4 ANSWER 33 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **172522-28-0** REGISTRY
CN DNA (hepatitis B virus clone H2 gene X protein cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (hepatitis B virus clone H2 gene X protein messenger RNA-complementary plus 5'- and 3'-flanking region fragment)
SQL 3207
MF Unspecified
CI MAN

REFERENCE 1: 124:78685

L4 ANSWER 34 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **172522-26-8** REGISTRY
CN DNA (hepatitis B virus clone E88 gene X protein cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (hepatitis B virus clone E88 gene X protein messenger RNA-complementary plus 5'- and 3'-flanking region fragment)
SQL 3192
MF Unspecified
CI MAN

REFERENCE 1: 124:78685

L4 ANSWER 35 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **168119-01-5** REGISTRY
CN DNA, d(G-C-C-C-C-A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(G-C-C-C-C-A-A-A-G-C-C-A-C-C-C-A-A-G-G-C-A)
SQL 21
MF Unspecified
CI MAN

REFERENCE 1: 128:226228

REFERENCE 2: 123:218381

L4 ANSWER 36 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **148188-81-2** REGISTRY
CN DNA (hepatitis B virus subtype ayw core antigen gene plus flanks) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (hepatitis B virus subtype ayw core antigen gene plus 5'- and 3'-flanking region fragment)
OTHER NAMES:
CN 63: PN: WO2005014806 PAGE: 52 unclaimed DNA
CN 8: PN: WO2004011624 PAGE: 60 unclaimed DNA
CN GenBank J02203 (Secondary GenBank Accession Number)
CN GenBank V01460
SQL 3182
MF Unspecified
CI MAN

REFERENCE 1: 142:234475

REFERENCE 2: 140:158524

REFERENCE 3: 124:1994

L4 ANSWER 37 OF 37 REGISTRY COPYRIGHT 2005 ACS on STN
RN **73247-02-6** REGISTRY
CN DNA (hepatitis B virus subtype ayw) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (hepatitis B virus subtype ayw)
SQL 3182
MF Unspecified
CI MAN

REFERENCE 1: 112:192774

REFERENCE 2: 92:141944

(FILE 'MEDLINE, BIOSIS, EMBASE' ENTERED AT 10:28:10 ON 05 APR 2005)
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